

SEQUENCE LISTING

<110> Snutch, Terry P.
Baillie, David L.

<120> NOVEL HUMAN CALCIUM CHANNELS AND RELATED PROBES, CELL
LINES AND METHODS

<130> NMED.P-001-2 (CIP)

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<151> 1998-02-25

<150> 60/039,204

<151> 1997-02-28

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<170> PatentIn Ver. 2.0

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Glu Asn Arg Leu Arg Asp Leu Gly Trp Val Ser Leu Glu Cys Gln Gly		
1475	1480	1485
Lys Val Gly Asp Leu Val Val Trp Val Tyr Gly Gln Arg Arg Gln Arg		
1490	1495	1500
Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu Ala Phe		
1505	1510	1515 1520
Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu		
1525	1530	1535
Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe		
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Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly		
1555	1560	1565
Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu		

1570	1575	1580	
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1585	1590	1595	1600
Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg			
	1605	1610	1615
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly			
	1620	1625	1630
Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly			
	1635	1640	1645
Asn Ile Val Leu Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu			
	1650	1655	1660
Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp			
	1665	1670	1675
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	1685	1690	1695
Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met			
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Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr			
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Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His			
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Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser			
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Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His			
	1765	1770	1775
Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu			
	1780	1785	1790
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Arg Leu			
	1795	1800	1805
Pro Tyr Tyr Ala Thr Tyr Cys His Thr Arg Leu Leu Ile His Ser Met			
	1810	1815	1820
Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu			

1825 1830 1835 1840

Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
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<210> 19
<211> 567
<212> DNA
<213> HUMAN

<220>
<223> human alpha-I partial sequence

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<213> HUMAN

<220>
<223> human alpha-I partial sequence

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20 25 30
Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
35 40 45
Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
50 55 60
Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp

65		70		75		80
Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly						
	85		90		95	
Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly						
	100		105		110	
Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr						
	115		120		125	
Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly Ala Ile						
	130		135		140	
Ser Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile						
	145		150		155	160
Thr Leu Glu Gly Trp Val Ala Ile Met Tyr Tyr Val Met Asp Ala Leu						
		165		170		175
Ser Phe Tyr Asn Phe Val Tyr Phe Ile Leu Leu Ile Ile						
	180		185			

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 <212> DNA
 <213> rat

<220>
 <223> rat alpha-I partial sequence

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 ttcactact tcactctgct tatcata 567

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 <212> PRT
 <213> rat

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<223> rat alpha-I partial sequence

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5

10

15

Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile

20

25

30

Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu

35

40

45

Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln

50

55

60

Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp

65

70

75

80

Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly

85

90

95

Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly

100

105

110

Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr

115

120

125

Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile

130

135

140

Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile

145

150

155

160

Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His

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170

175

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185

<210> 23

<211> 7540

<212> DNA

<213> rat

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<211> 2287

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<400> 24

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35 40 45

Pro Val Ala Ser Arg Ser Ser Thr Thr Cys Pro Gly Pro Gly Ala Ala
50 55 60

Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
835 840 845

Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
850 855 860

Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
865 870 875 880

Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
885 890 895

Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
900 905 910

Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
915 920 925

Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
930 935 940

Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
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Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
965 970 975

Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
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995 1000 1005

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1010 1015 1020

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Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln Pro Glu
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Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser Met
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Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro Leu Gly
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Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu Ala		
1140	1145	1150
Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe Thr		

1155	1160	1165
Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly Leu		
1170	1175	1180
Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Thr Asp Trp Asn Val Leu Asp		
1185	1190	1195 1200
Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Val Ala		
1205	1210	1215
Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Leu Leu Arg Thr		
1220	1225	1230
Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val		
1235	1240	1245
Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu		
1250	1255	1260
Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu		
1265	1270	1275 1280
Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp Thr Arg Asn Ile		
1285	1290	1295
Thr Asn Arg Ser Asp Cys Val Ala Ala Asn Tyr Arg Trp Val His His		
1300	1305	1310
Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu Phe Val		
1315	1320	1325
Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr Asn Gly Leu Asp		
1330	1335	1340
Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His Asn Pro Trp Met		
1345	1350	1355 1360
Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu		
1365	1370	1375
Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys Arg Gln		
1380	1385	1390
His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg		
1395	1400	1405
Arg Leu Glu Lys Lys Arg Arg Tyr Ala Gln Arg Leu Pro Tyr Tyr Ala		

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1665	1670	1675	1680
Val Leu Met Lys His Leu Asp Asp Ser Asn Lys Glu Ala Gln Glu Asp			
1685	1690	1695	
Ala Glu Met Asp Ala Glu Ile Glu Leu Glu Met Ala His Gly Ser Gly			
1700	1705	1710	
Pro Cys Pro Gly Pro Cys Pro Gly Pro Cys Pro Cys Pro Cys Pro Cys			
1715	1720	1725	
Pro Cys Ser Gly Pro Arg Cys Pro Leu Val Thr Trp Gly Ser Gly Ala			
1730	1735	1740	
Met Asp Arg Glu Gly Gln Val Leu Glu Ala His Arg Glu Ser Pro Val			
1745	1750	1755	1760
Arg Thr Ala Ile Arg Cys Trp Thr Pro Arg Val Thr Cys Ala Gly Thr			
1765	1770	1775	
Ala Ile Leu Gln Pro Arg Arg Pro Cys Gly Trp Thr Gly Ser Leu Glx			
1780	1785	1790	

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 <211> 540
 <212> DNA
 <213> rat

<400> 29
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 gctcagcagc ccagtggccc gtagtgggca ggagccccag ccagtggca gctgcactcg 180
 ctacacacct cgtctgtctg tccaccacct ggtccaccac catcaccacc accatcacca 240
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<210> 30
 <211> 2212
 <212> DNA
 <213> HUMAN

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<400> 30
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<210> 31
<211> 644
<212> PRT
<213> HUMAN

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 20 25 30
 Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
 35 40 45
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
 50 55 60
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
 65 70 75 80
 Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
 85 90 95
 Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
 100 105 110
 Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
 115 120 125
 Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
 130 135 140
 Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
 145 150 155 160
 Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
 165 170 175
 Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
 180 185 190
 Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
 195 200 205
 Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
 210 215 220
 Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
 225 230 235 240
 Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
 245 250 255
 Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
 260 265 270

Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
 275 280 285

Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
 290 295 300

Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
 305 310 315 320

Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
 325 330 335

Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
 340 345 350

Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
 355 360 365

Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
 370 375 380

Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
 385 390 395 400

Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
 405 410 415

Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
 420 425 430

Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
 435 440 445

Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
 450 455 460

Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
 465 470 475 480

Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
 485 490 495

His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
 500 505 510

Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
 515 520 525

Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
530 535 540

Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545 550 555 560

Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
565 570 575

Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590

Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605

Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620

Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
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Thr Gly Ala Cys

<210> 32

<211> 1608

<212> DNA

<213> HUMAN

<400> 32

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<210> 33
 <211> 518
 <212> PRT
 <213> HUMAN

<400> 33
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 Pro Gly Ala Pro Gly Arg Glu Ala Glu Arg Gly Ser Glu Leu Gly Val
 35 40 45
 Ser Pro Ser Glu Ser Pro Ala Ala Glu Arg Gly Ala Glu Leu Gly Ala
 50 55 60
 Asp Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe
 65 70 75 80
 Phe Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu
 85 90 95
 Val Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu
 100 105 110
 Asn Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys
 115 120 125
 Gly Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe
 130 135 140
 Ala Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu
 145 150 155 160
 Phe Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe

	165		170		175
Phe Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn					
	180		185		190
Val Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg					
	195		200		205
Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu					
	210		215		220
Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val					
	225		230		235
Phe Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu					
	245		250		255
Arg Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu					
	260		265		270
Thr Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro					
	275		280		285
Phe Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His					
	290		295		300
Ile Pro Gly Arg Arg Glu Leu Arg Met Pro Cys Thr Leu Gly Trp Glu					
	305		310		315
Ala Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala					
	325		330		335
Cys Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser					
	340		345		350
Asn Pro His Asn Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp					
	355		360		365
Ile Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met					
	370		375		380
Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile					
	385		390		395
Leu Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val					
	405		410		415
Val Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu					

430

<210> 35
<211> 359

<212> PRT
<213> HUMAN

<400> 35

Ser Val Met Ser Leu Gly Arg Met Ser Tyr Asp Gln Arg Ser Leu Ser
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Ser Ser Arg Ser Ser Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp
20 25 30

Ala Ser Arg Arg Ser Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser
35 40 45

Ala Glu His Glu Ser Leu Leu Ser Ala Glu Arg Gly Gly Gly Ala Arg
50 55 60

Val Cys Glu Val Ala Ala Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu
65 70 75 80

His Thr Pro His Ala His His Ile His His Gly Pro His Leu Ala His
85 90 95

Arg His Arg His His Arg Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser
100 105 110

Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly Ala His Pro Arg Ala
115 120 125

Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly
130 135 140

Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg
145 150 155 160

Gly Asp Arg Gly Glu Asp Glu Glu Glu Ile Asp Tyr Thr Leu Cys Phe
165 170 175

Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp Trp Cys Glu Val
180 185 190

Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu Asn Arg Phe Arg
195 200 205

Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val
210 215 220

Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro
225 230 235 240

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) \delta(x-a) dx = f(a)$

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

[illegible][illegible][illegible]

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) \delta(x-a) dx = f(a)$